

FIGURE 1

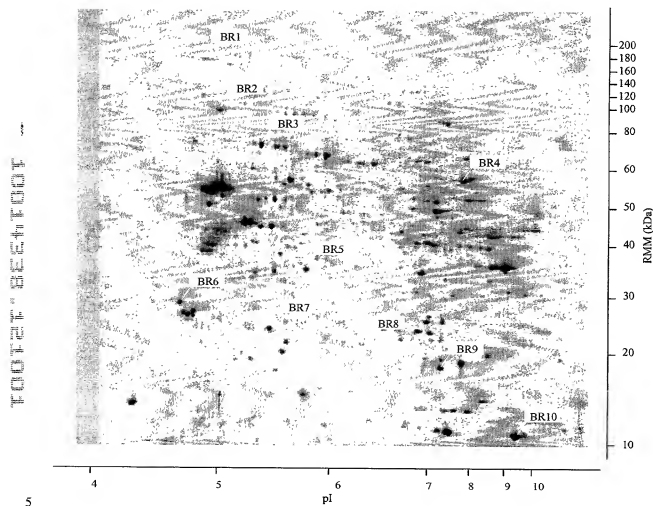


FIGURE 2.

Figure 2a

1 gtccgggacc atgtctggag aactaccacc aaacattaac atcaaggaac
5 51 ctcgatggga tcaaagcact ttcatggac gagccaatca tttcttcact
101 gtaactgacc ccaggaacat tctgttaacc aacgaacaac tcgagagtgc
151 gagaaaaata gtacatgatt acaggcaagg aattgttctt cctggtctta
201 cagaaaatga attgtggaga gcaaagtaca tctatgattc agcttttcac
251 cctgacactg gtgagaagat gattttgata ggaagaatgt cagcccagggt
0 301 tcccatgaac atgaccatca cagggtgtat gatgacgttt tacaggacta
351 cgccggctgt gctgttctgg cagtggatta accagtcctt caatgccgtc
401 gtcaattaca ccaacagaag tggagacgca cccctcactg tcaatgagtt
451 gggaaacagct tacgtttctg caacaactgg tgccgtagca acagctctag
501 gactcaatgc attgaccaag catgtctcac cactgatagg acgttttgtt
5 551 ccctttgtctg ccgtagctgc tgctaattgc attaatattc cattaatgag
601 gcaaagggaa ctcaaagttg gcattcccgt cacggatgag aatgggaacc
651 gcttggggga gtccggcgaac gctgcgaaac aagccatcac gcaagttgtc
701 gtgtccagga ttctcatggc agccctggc atggccatcc ctccattcat
751 tatgaacact ttggaaaaga aagcctttt gaagaggttc ccatggatga
20 801 gtgcacccat tcaagttggg ttagttggct tctgtttggt gtttgcata
851 ccctgtgtt gtgccctgtt tcctcagaaa agttccatgt ctgtgacaag
901 cttggaggcc gagtggcaag ctaagatcca agagagccat cctgaattgc
951 gacgcgtgta cttcaataag ggattgtaaa gcaggaggga aacctctgca
1001 gctcattctg ccactgcaa gctggtgtag ccatgctggt gagaaaaatc
25 1051 ctgttcaacc tgggttctcc cagttacgga aagggcgaat tcgcggccgc
1101 taattcgatt cgccctatag nagtngtaac antic

Figure 2b

- 1 MSGELPPNIN IKEPRWDQST FIGRANHFFT VTDPNRILLT NEQLESARKI
 51 VHDYRQGIVP PGLTENELWR AKYIYDSARH PDTSEKMILI GRMSAQVPMN
 5 101 MTITGCMITF YRTTPAVLFW QWINQSFNAV VNYTNREGDA PLTVNELGTA
 151 YVSATIGAVA TALGLNALTG HVSPLEGREV PFAAVAAANG INIPLMRQRE
 201 LKVGIPVTDE NGNRLGESAN AAKQAITQVV VSRILMAAPG MAIPPFIMNT
 251 LEKKAFLKRF PWMSAPIQVG LVGFCLVFAT PLCCALFPQK SSMSVTSLEA
 301 ELQAKIQESH PELRRVYFNK GL*
- 10 The tryptic peptides identified by mass spectrometry are underlined, motifs conserved in mouse sideroflexin I are boxed and sequences shaded in grey represent predicted transmembrane domains (Fleming *supra*)

FIGURE 3.

Figure 3a

1 gtcgggacc atgtctggag aactaccacc aacattaac atcaaggaac
5 51 ctcgatggga tcaaagcact ttcattggac gagccaatca tttcttact
101 gtaactgacc ccaggaacat tctgttaacc aacgaacaac tcgagagtgc
151 gagaaaaata gtacatgatt acaggcaagg aattgttcct cctgggtctta
201 cagaaaatga attgtggaga gcaaagtaca tctatgatcc agcttttcat
251 cctgacactg gtgagaagat gattttgata ggaagaatgt cagcccagggt
301 tcccatgaac atgaccatca cagggtgtat gatgacgttt tacaggacta
351 cgccggctgt gctgttctgg cagtggatta accagtcctt caatgccgtc
401 gtcaattaca ccaacagaag tggagacgca cccctcactg tcaatgagtt
451 gggaacagct tacgtttctg taacaactgg tgccgtagca acagctctag
501 gactcaatgc attgaccaag catgtctcac cactgatagg acgttttgtt
551 ccctttgctg ccgtagctgc tgctaattgc attaatattc cattaatgag
601 gcaaagccat ccctccattc attatgaaca ctttgaaaaa gaaagccttt
651 ttgaagaggt tcccatggat gagtgcaccc attcaagttg ggtagttgg
701 cttctgtttg gtgtttgcta caccctgtg ttgtgccctg tttctcaga
751 aaagtcccat gtctgtgaca agcttggagg ccgagttgca agctaagatc
20 801 caagagagcc atcctgaatt gcgacgcgtg tacttcaata agggattgta
851 aagcagggag gaaacctctg cagctcattc tgccactgca aagctgggtg
901 agccatgctg gtgagaaaaa tcctgttcaa cctgggttct ccagttang
951 gaaagggcga attcgcggcc gctgattcna ttac

Figure 3b

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5 1   MSGELPPNIN IKEPRWDQST FIGRANHFFT VTDERNILLT NEQLESARKI
51  VHDYRQGIVP PGLTENELWR AKYIYDSARH PDTSEKMILI GRMSANOVPMN
101 MTFITGCMMTF YRTTPAVIEW QWINSFNAV VNYTNBSGDA PLTVNELGTA
151 VVSVITGAVA TALGLNALTK HVSPLIGREV PFAAVAAANC INIPLMRQSH
201 PSIHYEHFGK ESLFEEVPMD ECTHSSWVSW LLFGVCYTPV LCPVSSEKFH
10 251 VCDKLGGRVA S*

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The tryptic peptides identified by mass spectrometry are underlined, motifs conserved in mouse sideroflexin I are boxed and amino acids unique to this clone are shown in bold (all other amino acids are identical to the full length clone), sequences shaded in grey represent the predicted transmembrane domains.